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            RAW SEQUENCE LISTING              DATE: 05/25/2004
            PATENT APPLICATION:  US/10/849,106    TIME: 08:04:06

            Input Set : N:\Crf3\RULE60\10849106.raw
            Output Set: N:\CRF4\05252004\J849106.raw

   1 <110> APPLICANT: Udagawa, Hiroaki
   2        Frandsen, Torben
   3        Nielsen, Tom
   4        Kauppinen, Markus
   5        Christensen, Soeren
   6 <120> TITLE OF INVENTION: Lysophospholipase
   7 <130> FILE REFERENCE: 5958.210-US
   8 <140> CURRENT APPLICATION NUMBER: US/10/849,106
   9 <141> CURRENT FILING DATE: 2004-05-19
  10 <150> PRIOR APPLICATION NUMBER: US/09/687,538
  11 <151> PRIOR FILING DATE: 2000-10-13
  12 <160> NUMBER OF SEQ ID NOS: 19
  13 <170> SOFTWARE: PatentIn version 3.1
  15 <210> SEQ ID NO: 1
  16 <211> LENGTH: 1923
  17 <212> TYPE: DNA
  18 <213> ORGANISM: Aspergillus niger
  19 <220> FEATURE:
  20 <221> NAME/KEY: CDS
  21 <222> LOCATION: (1)..(1920)
  22 <223> OTHER INFORMATION:
  23 <221> NAME/KEY: sig_peptide
  24 <222> LOCATION: (1)..(63)
  25 <223> OTHER INFORMATION:
W--> 26 <221> mat_peptide
  27 <222> LOCATION: (109)..()
  28 <223> OTHER INFORMATION:
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  30        atg aag ttc aat gca ctc tta acg acc ctc gcg gcg ctg ggg tat atc       48
  31        Met Lys Phe Asn Ala Leu Leu Thr Thr Leu Ala Ala Leu Gly Tyr Ile
  32            -35             -30             -25
  33        caa gga ggc gcc gcg gtt cct aca acc gtc gac ctc aca tat gca gac       96
  34        Gln Gly Gly Ala Ala Val Pro Thr Thr Val Asp Leu Thr Tyr Ala Asp
  35        -20             -15             -10                 -5
  36        ata tca cct cgc gca ctg gat aat gcc cct gat ggt tat acc ccg agc      144
  37        Ile Ser Pro Arg Ala Leu Asp Asn Ala Pro Asp Gly Tyr Thr Pro Ser
  38                    -1  1               5                   10
  39        aat gta tcc tgt cct gca aac aga ccg acg att cgc agc gcg tca acc      192
  40        Asn Val Ser Cys Pro Ala Asn Arg Pro Thr Ile Arg Ser Ala Ser Thr
  41                    15              20              25
  42        ctg tca tcg aac gag acg gca tgg gtg gac gtc cgg cgt aag cag act      240
  43        Leu Ser Ser Asn Glu Thr Ala Trp Val Asp Val Arg Arg Lys Gln Thr
  44            30              35              40
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45    gtc tca gcg atg aaa gac ctt ttc ggc cat atc aac atg agc tca ttt    288
46    Val Ser Ala Met Lys Asp Leu Phe Gly His Ile Asn Met Ser Ser Phe
47    45                      50                  55                  60
48    gac gct att tcg tac atc aac agc cat tca tca aat atc acc aac ata    336
49    Asp Ala Ile Ser Tyr Ile Asn Ser His Ser Ser Asn Ile Thr Asn Ile
50                        65                  70                  75
51    ccc aac atc ggt att gcc gtg tcc ggc ggt ggc tac aga gcc ctg acc    384
52    Pro Asn Ile Gly Ile Ala Val Ser Gly Gly Gly Tyr Arg Ala Leu Thr
53                    80                  85                  90
54    aac ggc gcg gga gca ctc aag gca ttc gac agt cga acg gaa aac tca    432
55    Asn Gly Ala Gly Ala Leu Lys Ala Phe Asp Ser Arg Thr Glu Asn Ser
56                95                  100                 105
57    acc cat aat gga cag ctc ggt ggt ctt ctg cag tca gcc aca tac ctg    480
58    Thr His Asn Gly Gln Leu Gly Gly Leu Leu Gln Ser Ala Thr Tyr Leu
59        110                 115                 120
60    tcc ggt ctc tcc gga ggt ggc tgg ctc ctg ggc tca atc tac atc aac    528
61    Ser Gly Leu Ser Gly Gly Gly Trp Leu Leu Gly Ser Ile Tyr Ile Asn
62    125                 130                 135                 140
63    aac ttc acc acc gtc tcc aat ctg caa acc tac aaa gag ggc gaa gtc    576
64    Asn Phe Thr Thr Val Ser Asn Leu Gln Thr Tyr Lys Glu Gly Glu Val
65                    145                 150                 155
66    tgg cag ttc cag aat tca atc acg aaa ggc cca aag acc aac ggc ttg    624
67    Trp Gln Phe Gln Asn Ser Ile Thr Lys Gly Pro Lys Thr Asn Gly Leu
68                160                 165                 170
69    caa gct tgg gat aca gcc aag tac tac cgc gat ctg gcc aag gtg gtc    672
70    Gln Ala Trp Asp Thr Ala Lys Tyr Tyr Arg Asp Leu Ala Lys Val Val
71                175                 180                 185
72    gct ggc aag aag gac gcg ggc ttc aac act tcc ttc acg gac tac tgg    720
73    Ala Gly Lys Lys Asp Ala Gly Phe Asn Thr Ser Phe Thr Asp Tyr Trp
74        190                 195                 200
75    ggt cgc gca ctc tcc tac cag ctg att aac gcg acc gac gga ggc cca    768
76    Gly Arg Ala Leu Ser Tyr Gln Leu Ile Asn Ala Thr Asp Gly Gly Pro
77    205                 210                 215                 220
78    ggc tac acc tgg tca tcg atc gct tta acc cag ggc ttc aag aac gga    816
79    Gly Tyr Thr Trp Ser Ser Ile Ala Leu Thr Gln Gly Phe Lys Asn Gly
80                    225                 230                 235
81    aac atg ccc atg ccg ctc ctt gtc gcc gac ggc cgc aac cca ggc gag    864
82    Asn Met Pro Met Pro Leu Leu Val Ala Asp Gly Arg Asn Pro Gly Glu
83                240                 245                 250
84    acc cta atc ggc agc aac tcg acc gtg tat gag ttc aac ccc tgg gaa    912
85    Thr Leu Ile Gly Ser Asn Ser Thr Val Tyr Glu Phe Asn Pro Trp Glu
86        255                 260                 265
87    ttc ggc agt ttt gat ccg tcc atc ttc ggc ttc gct ccc ctc gaa tac    960
88    Phe Gly Ser Phe Asp Pro Ser Ile Phe Gly Phe Ala Pro Leu Glu Tyr
89        270                 275                 280
90    ctc gga tcc tac ttt gag aac ggc gaa gtc cca tcc agc cga tcc tgc    1008
91    Leu Gly Ser Tyr Phe Glu Asn Gly Glu Val Pro Ser Ser Arg Ser Cys
92    285                 290                 295                 300
93    gtc cgc ggc ttc gat aac gca ggc ttc gtc atg gga acc tcc tcc agt    1056
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Input Set : N:\Crf3\RULE60\10849106.raw
Output Set: N:\CRF4\05252004\J849106.raw

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94    Val Arg Gly Phe Asp Asn Ala Gly Phe Val Met Gly Thr Ser Ser Ser
95                    305                 310                 315
96    ctc ttc aac caa ttc atc ctg aag ctc aac acc acc gac atc cca tca   1104
97    Leu Phe Asn Gln Phe Ile Leu Lys Leu Asn Thr Thr Asp Ile Pro Ser
98                    320                 325                 330
99    acc ctc aaa acg gtc atc gcc agc atc cta gaa gaa cta ggc gac cgc   1152
100    Thr Leu Lys Thr Val Ile Ala Ser Ile Leu Glu Glu Leu Gly Asp Arg
101                   335                 340                 345
102    aac gac gac atc gcc atc tac tct ccc aac ccc ttc tac ggg tac cgc   1200
103    Asn Asp Asp Ile Ala Ile Tyr Ser Pro Asn Pro Phe Tyr Gly Tyr Arg
104       350                 355                 360
105    aac gcg aca gtt tca tac gaa aag acc ccg gac ctg aac gtc gtc gac   1248
106    Asn Ala Thr Val Ser Tyr Glu Lys Thr Pro Asp Leu Asn Val Val Asp
107    365                 370                 375                 380
108    ggt ggc gaa gac aaa cag aac ctc ccc ctc cat cct ctc atc caa ccc   1296
109    Gly Gly Glu Asp Lys Gln Asn Leu Pro Leu His Pro Leu Ile Gln Pro
110                   385                 390                 395
111    gcc cgc aac gtg gac gtc atc ttc gcc gtc gac tcc tca gcc agt acc   1344
112    Ala Arg Asn Val Asp Val Ile Phe Ala Val Asp Ser Ser Ala Ser Thr
113                   400                 405                 410
114    tcg gac aac tgg ccc aac gga agt cct ctc gtc gcg act tac gaa cgt   1392
115    Ser Asp Asn Trp Pro Asn Gly Ser Pro Leu Val Ala Thr Tyr Glu Arg
116                   415                 420                 425
117    agt ctc aac tca acc ggt atc gga aac ggc acc gcg ttc cct agc atc   1440
118    Ser Leu Asn Ser Thr Gly Ile Gly Asn Gly Thr Ala Phe Pro Ser Ile
119                   430                 435                 440
120    ccg gac aag agc acc ttc att aac ctg ggc ttg aac acc cgt ccg act   1488
121    Pro Asp Lys Ser Thr Phe Ile Asn Leu Gly Leu Asn Thr Arg Pro Thr
122    445                 450                 455                 460
123    ttc ttc ggc tgc aat agt tcc aat atc aca ggc cat gca ccc ctg gtt   1536
124    Phe Phe Gly Cys Asn Ser Ser Asn Ile Thr Gly His Ala Pro Leu Val
125                   465                 470                 475
126    gtc tac ctc ccc aac tac ccc tac aca acc ctc tcc aac aag tcg acc   1584
127    Val Tyr Leu Pro Asn Tyr Pro Tyr Thr Thr Leu Ser Asn Lys Ser Thr
128                   480                 485                 490
129    ttc cag ctc aag tac gag atc ttg gag cgt gat gag atg atc acc aat   1632
130    Phe Gln Leu Lys Tyr Glu Ile Leu Glu Arg Asp Glu Met Ile Thr Asn
131                   495                 500                 505
132    ggc tgg aac gtg gtt act atg ggt aat gga tca agg aag tct tac gag   1680
133    Gly Trp Asn Val Val Thr Met Gly Asn Gly Ser Arg Lys Ser Tyr Glu
134       510                 515                 520
135    gat tgg ccg act tgt gcg ggc tgc gct att ctg agt cgc tcg ttt gat   1728
136    Asp Trp Pro Thr Cys Ala Gly Cys Ala Ile Leu Ser Arg Ser Phe Asp
137    525                 530                 535                 540
138    cgg act aat acc cag gtg ccg gat atg tgc tcg cag tgt ttt gac aag   1776
139    Arg Thr Asn Thr Gln Val Pro Asp Met Cys Ser Gln Cys Phe Asp Lys
140                   545                 550                 555
141    tat tgc tgg gat gga acg agg aat agt acg acg ccg gcg gcg tat gag   1824
142    Tyr Cys Trp Asp Gly Thr Arg Asn Ser Thr Thr Pro Ala Ala Tyr Glu
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143                560              565              570
144    ccg aag gta ttg atg gct agt gcg ggt gtg agg ggt att tcg atg tcg   1872
145    Pro Lys Val Leu Met Ala Ser Ala Gly Val Arg Gly Ile Ser Met Ser
146                575              580              585
147    agg ttg gtt ttg ggt ctc ttt ccg gtg gtg gtt ggg gtt tgg atg atg   1920
148    Arg Leu Val Leu Gly Leu Phe Pro Val Val Val Gly Val Trp Met Met
149                590              595              600
150    tga                                                               1923
152 <210> SEQ ID NO: 2
153 <211> LENGTH: 640
154 <212> TYPE: PRT
155 <213> ORGANISM: Aspergillus niger
156 <400> SEQUENCE: 2
157    Met Lys Phe Asn Ala Leu Leu Thr Thr Leu Ala Ala Leu Gly Tyr Ile
158        -35              -30              -25
159    Gln Gly Gly Ala Ala Val Pro Thr Thr Val Asp Leu Thr Tyr Ala Asp
160    -20              -15              -10                       -5
161    Ile Ser Pro Arg Ala Leu Asp Asn Ala Pro Asp Gly Tyr Thr Pro Ser
162             -1  1              5                        10
163    Asn Val Ser Cys Pro Ala Asn Arg Pro Thr Ile Arg Ser Ala Ser Thr
164             15               20               25
165    Leu Ser Ser Asn Glu Thr Ala Trp Val Asp Val Arg Arg Lys Gln Thr
166        30               35               40
167    Val Ser Ala Met Lys Asp Leu Phe Gly His Ile Asn Met Ser Ser Phe
168    45               50               55                        60
169    Asp Ala Ile Ser Tyr Ile Asn Ser His Ser Ser Asn Ile Thr Asn Ile
170             65               70               75
171    Pro Asn Ile Gly Ile Ala Val Ser Gly Gly Gly Tyr Arg Ala Leu Thr
172             80               85               90
173    Asn Gly Ala Gly Ala Leu Lys Ala Phe Asp Ser Arg Thr Glu Asn Ser
174             95               100              105
175    Thr His Asn Gly Gln Leu Gly Gly Leu Leu Gln Ser Ala Thr Tyr Leu
176        110              115              120
177    Ser Gly Leu Ser Gly Gly Gly Trp Leu Leu Gly Ser Ile Tyr Ile Asn
178    125              130              135                       140
179    Asn Phe Thr Thr Val Ser Asn Leu Gln Thr Tyr Lys Glu Gly Glu Val
180             145              150              155
181    Trp Gln Phe Gln Asn Ser Ile Thr Lys Gly Pro Lys Thr Asn Gly Leu
182             160              165              170
183    Gln Ala Trp Asp Thr Ala Lys Tyr Tyr Arg Asp Leu Ala Lys Val Val
184             175              180              185
185    Ala Gly Lys Lys Asp Ala Gly Phe Asn Thr Ser Phe Thr Asp Tyr Trp
186        190              195              200
187    Gly Arg Ala Leu Ser Tyr Gln Leu Ile Asn Ala Thr Asp Gly Gly Pro
188    205              210              215                       220
189    Gly Tyr Thr Trp Ser Ser Ile Ala Leu Thr Gln Gly Phe Lys Asn Gly
190             225              230              235
191    Asn Met Pro Met Pro Leu Leu Val Ala Asp Gly Arg Asn Pro Gly Glu
192             240              245              250
```

```
193        Thr Leu Ile Gly Ser Asn Ser Thr Val Tyr Glu Phe Asn Pro Trp Glu
194                255                 260                 265
195        Phe Gly Ser Phe Asp Pro Ser Ile Phe Gly Phe Ala Pro Leu Glu Tyr
196            270                 275                 280
197        Leu Gly Ser Tyr Phe Glu Asn Gly Glu Val Pro Ser Ser Arg Ser Cys
198        285                 290                 295                 300
199        Val Arg Gly Phe Asp Asn Ala Gly Phe Val Met Gly Thr Ser Ser Ser
200                305                 310                 315
201        Leu Phe Asn Gln Phe Ile Leu Lys Leu Asn Thr Thr Asp Ile Pro Ser
202                320                 325                 330
203        Thr Leu Lys Thr Val Ile Ala Ser Ile Leu Glu Glu Leu Gly Asp Arg
204                335                 340                 345
205        Asn Asp Asp Ile Ala Ile Tyr Ser Pro Asn Pro Phe Tyr Gly Tyr Arg
206            350                 355                 360
207        Asn Ala Thr Val Ser Tyr Glu Lys Thr Pro Asp Leu Asn Val Val Asp
208        365                 370                 375                 380
209        Gly Gly Glu Asp Lys Gln Asn Leu Pro Leu His Pro Leu Ile Gln Pro
210                385                 390                 395
211        Ala Arg Asn Val Asp Val Ile Phe Ala Val Asp Ser Ser Ala Ser Thr
212                400                 405                 410
213        Ser Asp Asn Trp Pro Asn Gly Ser Pro Leu Val Ala Thr Tyr Glu Arg
214                415                 420                 425
215        Ser Leu Asn Ser Thr Gly Ile Gly Asn Gly Thr Ala Phe Pro Ser Ile
216            430                 435                 440
217        Pro Asp Lys Ser Thr Phe Ile Asn Leu Gly Leu Asn Thr Arg Pro Thr
218        445                 450                 455                 460
219        Phe Phe Gly Cys Asn Ser Ser Asn Ile Thr Gly His Ala Pro Leu Val
220                465                 470                 475
221        Val Tyr Leu Pro Asn Tyr Pro Tyr Thr Thr Leu Ser Asn Lys Ser Thr
222                480                 485                 490
223        Phe Gln Leu Lys Tyr Glu Ile Leu Glu Arg Asp Glu Met Ile Thr Asn
224                495                 500                 505
225        Gly Trp Asn Val Val Thr Met Gly Asn Gly Ser Arg Lys Ser Tyr Glu
226            510                 515                 520
227        Asp Trp Pro Thr Cys Ala Gly Cys Ala Ile Leu Ser Arg Ser Phe Asp
228        525                 530                 535                 540
229        Arg Thr Asn Thr Gln Val Pro Asp Met Cys Ser Gln Cys Phe Asp Lys
230                545                 550                 555
231        Tyr Cys Trp Asp Gly Thr Arg Asn Ser Thr Thr Pro Ala Ala Tyr Glu
232                560                 565                 570
233        Pro Lys Val Leu Met Ala Ser Ala Gly Val Arg Gly Ile Ser Met Ser
234                575                 580                 585
235        Arg Leu Val Leu Gly Leu Phe Pro Val Val Val Gly Val Trp Met Met
236            590                 595                 600
238 <210> SEQ ID NO: 3
239 <211> LENGTH: 1917
240 <212> TYPE: DNA
241 <213> ORGANISM: Aspergillus niger
242 <220> FEATURE:
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/25/2004
PATENT APPLICATION: **US/10/849,106**   TIME: 08:04:07

Input Set : **N:\Crf3\RULE60\10849106.raw**
Output Set: **N:\CRF4\05252004\J849106.raw**

<u>**Please Note:**</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 9
Seq#:13; N Pos. 3,6,9,15,18,24
Seq#:14; N Pos. 16,19

VERIFICATION SUMMARY   DATE: 05/25/2004
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Input Set : **N:\Crf3\RULE60\10849106.raw**
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L:26 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:29 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:249 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:249 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:0
L:249 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:0
L:468 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:468 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
L:471 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:471 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
L:471 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
L:688 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:688 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:0
L:688 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:0
L:911 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:914 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:916 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:917 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:925 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:927 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:936 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:938 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:947 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:949 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:958 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:961 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:964 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:967 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:970 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:973 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:976 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:978 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:987 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:990 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:993 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:995 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:996 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:1004 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1006 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:1015 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1017 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:1026 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1028 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:1037 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1039 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
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